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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/664,859	09/22/2003	Konrad Basler	Q-77377	4459

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SUGHRUE MION, PLLC
2100 Pennsylvania Avenue, NW
Washington, DC 20037-3213

EXAMINER

CARLSON, KAREN C

ART UNIT	PAPER NUMBER
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1653

DATE MAILED: 11/23/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/664,859

Applicant(s)

BASLER ET AL

Examiner

Karen Cochrane Carlson, Ph.D.

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on ____.
- 2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 61-66 is/are pending in the application.
- 4a) Of the above claim(s) ____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) ____ is/are allowed.
- 6) ☒ Claim(s) 61-66 is/are rejected.
- 7) ☐ Claim(s) ____ is/are objected to.
- 8) ☐ Claim(s) ____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on ____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. ____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|--|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. ____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>9/22/03</u> | 6) <input checked="" type="checkbox"/> Other: <u>3 SEQ attachments</u> |

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Claims 1-60 have been cancelled. New Claims 61-66 are currently pending and are under examination.

Priority is set to July 28, 2000.

Sequence Compliance:

There is no amino acid sequence identifier depicting the amino acid sequence depicted in Figure 2, or under the nucleotide sequence of SEQ ID NO: 1. Thus, the Sequence Rules have not been met.

Further, upon finding the art of Venter et al. (US PG Pub 2005/0208558), the search of polypeptides encoded by the nucleotide sequence of SEQ ID NO: 1 shows that Venter et al.'s SEQ ID NO: 3129 is identical to residues 6-1429 of this amino acid sequence, herein now to be referred to as SEQ ID NO: X to help prevent confusion of what is instant SEQ ID NO: 1 (a nucleotide sequence) versus what Applicants claim SEQ ID NO: 1 to be (both nucleotide and amino acid sequences). However, perusal of the C-terminal amino acids of SEQ ID NO: X shows that these amino acids correspond to the C-terminal of Venter et al.'s SEQ ID NO: 3129, that is, the string of amino acids N-terminal of residue 1464 is the same as Venter et al.'s string of amino acids N-terminal to residue 1429. Thus, there is a discrepancy of 40 amino acids (5 at the N-terminus of SEQ ID NO: 3129 and 40 somewhere in-between the N- and C-terminal of SEQ ID NO: X).

Venter et al.'s SEQ ID NO: 3129 is 1429 amino acid in length, of which amino acids 6-1429 are identical to the computer readable form of instant SEQ ID NO: X as determined by the Examiner's perusal of the sequence search. However, SEQ ID NO: X is 1464 amino acids long in paper form. Upon perusal of Venter et al.'s SEQ ID NO: 3129 and SEQ ID NO: X of the instant paper copy of the Sequence listing, amino acids 1140-1179 of the paper form of SEQ ID NO: X is

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missing in SEQ ID NO: 3129 at amino acid position 1144-1145 of SEQ ID NO: 3129. When the sequence search was reviewed again, the nucleotides encoding these same amino acids (nucleotides 5482-5601 of SEQ ID NO: 1) are missing from the computer readable form of instant SEQ ID NO: 1. Thus, the paper copy and the computer readable form of SEQ ID NO: 1 are not identical.

Thus:

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth above.

Applicants must comply with the sequence rules in response to this office or their response will be held non-responsive.

The disclosure is objected to because of the following informalities:

At page 1, para. 2, line 1, "cystein" should be written as --- cysteine ---.

At page 18 and 39, the sequence identifiers are not placed after the sequences.

At page 32, para. 2, line 4, "Cels" should be written as --- cells ---.

At page 10+, the figure legends must refer to "Figure 1(A), Figure 1(B), and so on, for example, because there is no figure "B" or "Figure 1" in the drawings. See also the legends for figures 3, 5, 7, 8, 10, 11, 12, 13, and 15.

Also, reference to the figures throughout the specification must refer to the specifically named figure. That is, at page 22, para. 3, Figure 1 is referred to instead of "Figure 1(A), for example. See also reference to Figure 7 at page 24, para. 2 and page 26, line 4; Figure 8 at page 27, line 8; and Figures 8 and 10 at page 30, para. 1, for example.

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It is noted that parent application 09/915,543 has been allowed. Upon issuance of this application the priority information at page 1 of the specification will have to be updated.

Appropriate correction is required.

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Hyperlinks can be found at pages 23, 29, and 41. Applicants should delete http:// to remove the hyperlink.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 61-66 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 61 and 62 refer to nucleotide sequence SEQ ID NO: 1 as both the nucleic acid encoding and the amino acid sequence depicting dlgs. Thus, it is not clear what sequence identifies the amino acid sequence. Additionally, Claim 61 refers to amino acids 1-1464 of SEQ ID NO: 1, while the computer readable form of the translation of SEQ ID NO: 1 depicts an amino acid sequence of 1429 amino acids (ie, SEQ ID NO: X).

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make

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and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 61-66 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 65 refers to chimeric polypeptides comprising dlgs (variants and fragments) and glutathione-S-transferase, thioredoxin, or an antibody. At page 6, para. 2 of the specification, the specification states that chimeric polypeptide will comprise dlgs (variants and fragments) and an epitope sequence tag, glutathione-S-transferase, beta-galactosidase, or alkaline phosphatase. Claim 65 is a new claim and is not part of the original disclosure. Thus, the inclusion of thioredoxin, or an antibody as being part of a chimeric polypeptide with dlgs (variants and fragments) is new matter.

Regarding written description, the specification does not describe variants of SEQ ID NO: X having at least 90% identity to SEQ ID NO: X, or biologically active fragments of SEQ ID NO: X. While the claims state that the fragments of SEQ ID NO: X will bind to an antibody against itself, this is not a biological activity, but rather a circular activity, that is, there is no reason for one of skill in the art to use an antibody to bind a fragment of SEQ ID NO: 1 if that fragment has no known activity.

Regarding the written description for dlgs fragments SEQ ID NO: 2, 4, 6, 8, or 10, SEQ ID NO: 2 has been shown to bind Doll (page 37). However, the specification fails to address any activity associated with SEQ ID NO: 4, 6, 8, or 10. Thus, without a correlation of structure to function, these sequences lack written description.

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The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

Claims 61, 62, 63, and 66 are rejected under 35 U.S.C. 102(e) as being anticipated by Venter et al. (Pub. No. US 2005/0208558). Venter et al.'s SEQ ID NO: 3129 is the same as SEQ ID NO: 3135 in Venter et al.'s provisional application 60/191,637, filed March 23, 2000.

Venter et al. teach SEQ ID NO: 3129, which encompasses amino acids 6-1429 of SEQ ID NO: X as shown in the sequence search (back translation of the computer readable form of SEQ ID NO: 1). Thus, for the purposes of this rejection in view of the noncompliance of the Sequence Rules as noted above, Venter et al. anticipate SEQ ID NO: X (Claims 61, 62), polypeptides having at least 90% identity to SEQ ID NO: X (Claim 61), and polypeptides comprising fragments of SEQ ID NO: X (Claim 61).

Even if the paper form of SEQ ID NO: X were used, the sequences would share 97.2% sequence identity (1423/1464; Claim 61).

Regarding fragments, SEQ ID N: 2, 4, 6, 8, and 10 can be found at amino acid positions 323-334, 520-554, 711-725, 760-768, and 773-884, respectively, in Venter et al.'s SEQ ID NO: 3129 (Claim 63).

At para.[0016] of Venter et al., these polypeptides are placed in pharmaceutical compositions (Claim 66).

No Claims are allowed.

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Any inquiry concerning this communication or earlier communications from the examiner should be directed to Karen Cochrane Carlson, Ph.D. whose telephone number is 571-272-0946.

The examiner can normally be reached on 7:00 AM - 4:00 PM, off alternate Fridays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Jon Weber can be reached on 571-272-0925. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



KAREN COCHRANE CARLSON, PH.D
PRIMARY EXAMINER

10/664 859 Attach #1

Marked up
Seq ID NO: 1
"MO: X"

SEQUENCE LISTING

<110> BASLER, Konrad
BRUNNER, Erich
FROESCH, Barbara
KRAMPS, Thomas
PETER, Oliver

<120> ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY AND THERAPEUTIC
AND DIAGNOSTIC APPLICATIONS BASED THEREON

<130> Q60361

<140> 09/915,543

<141> 2001-07-27

<150> 60/221,502

<151> 2000-07-28

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 6909

<212> DNA

<213> Drosophila lgs

<220>

<221> exon

<222> (691) .. (981)

<223>

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<223>

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<223>

[illegible]

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115 120 125 130	
act cag atg gta gat tgt gac gag caa tcg aag aaa aac aaa tgt agt	963
Thr Gln Met Val Asp Cys Asp Glu Gln Ser Lys Lys Asn Lys Cys Ser	
135 140 145	
gtg aag gac gag gaa gct ggtaagactg ccctacaaat ggtttaaaat	1011
Val Lys Asp Glu Glu Ala	
150	
tttaaaatgt attggcggtc acctttgtta atcatttaat tgtttttttt ttgctatact	1071
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Glu Ile Ser Ser Asn Lys Ala Lys Gly	
155 160	
caa gca gct ggt ggc ggc tgc gaa aca ggt tct aca tcc agt ttg act	1530
Gln Ala Ala Gly Gly Gly Cys Glu Thr Gly Ser Thr Ser Ser Leu Thr	
165 170 175	
gtc aag gaa gaa ccc acc gat gtc tta ggc agt tta gta aat atg aaa	1578
Val Lys Glu Glu Pro Thr Asp Val Leu Gly Ser Leu Val Asn Met Lys	
180 185 190	
aaa gaa gaa aga gaa aat cat tcg cca acg atg tcc cct gtt ggt ttt	1626
Lys Glu Glu Arg Glu Asn His Ser Pro Thr Met Ser Pro Val Gly Phe	
195 200 205	
ggg tca att ggt aat gca cag gac aac tcc gct aca ccg ggtaagtttt	1675
Gly Ser Ile Gly Asn Ala Gln Asp Asn Ser Ala Thr Pro	
210 215 220	
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tcg tcc ttg aca atg aat aat gac gaa atg agc atg gaa ggc tgc aat Ser Ser Leu Thr Met Asn Asn Asp Glu Met Ser Met Glu Gly Cys Asn 240 245 250	2489
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agc ggt caa ttt caa act att att gcg tat cac tgc act cag cct gct Ser Gly Gln Phe Gln Thr Ile Ile Ala Tyr His Cys Thr Gln Pro Ala 335 340 345 350	2777
aca aaa agc ttc ctg gaa gac ttt ttt atg aaa aac cct tta aag att Thr Lys Ser Phe Leu Glu Asp Phe Phe Met Lys Asn Pro Leu Lys Ile 355 360 365	2825
aac aag tta cag cgg cac aat tcc gtc ggt atg cca tgg ata ggc atg Asn Lys Leu Gln Arg His Asn Ser Val Gly Met Pro Trp Ile Gly Met 370 375 380	2873
ggg cag gtt gga cta act cct cct aat cct gta gcc aaa ata aca caa Gly Gln Val Gly Leu Thr Pro Pro Asn Pro Val Ala Lys Ile Thr Gln 385 390 395	2921

NO.2

cag cag cca cat aca aag acc gta ggc cta ttg aaa ccc caa ttc aat	2969
Gln Gln Pro His Thr Lys Thr Val Gly Leu Leu Lys Pro Gln Phe Asn	
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caa cat gaa aac agc aaa cgt agt act gta agc gcg cct agc aac tct	3017
Gln His Glu Asn Ser Lys Arg Ser Thr Val Ser Ala Pro Ser Asn Ser	
415 420 425 430	
ttt gtc gac cag tct gat cct atg ggc aac gaa act gaa ttg atg tgc	3065
Phe Val Asp Gln Ser Asp Pro Met Gly Asn Glu Thr Glu Leu Met Cys	
435 440 445	
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Trp Glu Gly Gly Ser Ser Asn Thr Ser Arg Ser Gly Gln Asn Ser Arg	
450 455 460	
aat cat gta gac agt atc agt aca tcc agc gag tca cag gca ata aag	3161
Asn His Val Asp Ser Ile Ser Thr Ser Ser Glu Ser Gln Ala Ile Lys	
465 470 475	
ata ctg gaa gca gct ggc gtt gat ttg gga cag gtc aca aaa gga agc	3209
Ile Leu Glu Ala Ala Gly Val Asp Leu Gly Gln Val Thr Lys Gly Ser	
480 485 490	
gat cct ggc ctg aca act gaa aac aac att gta tca ctg caa gga gtt	3257
Asp Pro Gly Leu Thr Thr Glu Asn Asn Ile Val Ser Leu Gln Gly Val	
495 500 505 510	
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Lys Val Pro Asp Glu Asn Leu Thr Pro Gln Gln Arg Gln His Arg Glu	
515 520 525	
gaa cag ttg gca aaa ata aaa aaa atg aat caa ttt ctt ttt cct gaa	3353
Glu Gln Leu Ala Lys Ile Lys Lys Met Asn Gln Phe Leu Phe Pro Glu	
530 535 540	
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Asn Glu Asn Ser Val Gly Ala Asn Val Ser Ser Gln Ile Thr Lys Ile	
545 550 555	
cca gga gat tta atg atg ggg atg tcg ggt ggc gga ggc gga tct att	3449
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5482 not in Ventner

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Asp Gly Ser Met Asn Ile Gly Gln Pro Ser Met Ile Arg Gly Met	
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: November 2, 2005, 22:10:58 ; Search time 876.5 Seconds

(without alignments)
6590.438 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 3730428

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcpt -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcpt -NORM=ext -HEAPSIZ=500 -MINLEN=0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	570	4.7	112	9	US-09-915-543-10
3	570	4.7	112	14	US-10-322-579-10
4	570	4.7	112	15	US-10-664-859-10
5	321.5	2.7	1335	15	US-10-276-774-2178
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7	314	2.6	1394	16	US-10-723-860-1764
8	314	2.6	1394	18	US-10-756-149-5163
9	312	2.6	1426	9	US-09-915-543-15
10	312	2.6	1426	14	US-10-322-579-15
11	312	2.6	1426	15	US-10-664-859-15
12	312	2.6	1426	16	US-10-408-765A-1958
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24	233.5	1.9	1243	16	US-10-408-765A-1964
25	233.5	1.9	1441	15	US-10-355-218-2
26	233.5	1.9	1441	15	US-10-503-050A-2
27	233	1.9	2703	20	US-11-097-143-16689
28	233	1.9	3190	17	US-10-733-923-18448
29	230.5	1.9	3375	18	US-10-840-060-90
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31	2230	1.9	3276	17	US-10-733-923-18447
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45	222.5	1.8	2440	18	US-10-885-977-35

ALIGNMENTS

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Sequence 3129, App1
US-11-097-143-3129 Application US/11097143
PubId: 11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: C1000728
CURRENT APPLICATION NUMBER: US/11/097,143
PRIOR FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/457,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769

Alignment #538
Attach #2

PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: 60/173,383
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/175,693
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/184,831
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/191,637
 PRIOR FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 4308
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 3129
 LENGTH: 1429
 TYPE: PRF
 ORGANISM: DROSOPHILA
 US-11-097-143-3129

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 Best Local Similarity: 71.04% Mismatches: 3
 Query Match: 58.49% Indels: 577
 DB: Gaps: 6

US-10-664-859-1 (1-6909) x US-11-097-143-3129 (1-1429)

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 QY 513 GCGTCCCAACATGATCTGATCAATCTGAGAGCGATCGGAATAGGAGACGCG 572
 DB 21 AlseSerThrmSerAlaSerGlySerAnProGlyAlaAlaIleGlyAnGlyAspSer 40
 QY 573 GCGCGAGACAAAGTTCTCGAGAACCTTAATAGCAACCTTTTCTACTTGTGCGCG 632
 DB 41 AlalaSerAlaSerSerProGlyThrluAnSerGluProPheSerThrluSer-- 59
 QY 633 GGTAAAGACTTGATTTCTCTTGTGCGGAATTATACACTTTCTGTGTTCCAGA 692
 DB 60 -----ProAs 61
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 DB 81 bAlaAlaIleThrGlyGlyAlaProGlySerGlyAlaAnSerLeuProGluGlyInThrmle 101
 QY 813 AAGGCAAGACTCTGAGACCAATCACTGCTGCTTGTCTGCAAAAACCTCGAG 872
 DB 101 uAGGInAnSerThrmSerThrlleAnSerCyleuValAlaSerProGlnAnSerSe 121
 QY 873 TGAACACTGCAATGAGCAATGCTGCTACAGTGGGCTTACTAGATGTAATG 932
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DB 157 ----- 157
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 QY 1413 AAAAGCTGCTATATATTCATTAACATTAATGTCATTTCAAGAAATTAAGTTCAATTA 1472
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 DB 163 bAlaIlyGlyGlnAlaIleGlyGlyCybGluThGlySerThrmSerSerLeuThrVa 183
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RESULT 2
US-09-915-543-10
; Sequence 10, Application US/09915543
; Publication No. US20020086986A1
; GENERAL INFORMATION:
; APPLICANT: BASLER, Konrad
; APPLICANT: BRUNNER, Erich

Attach #3



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<211> LENGTH: 1429

<212> TYPE: PRT

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<213> ORGANISM: DROSOPHILA

<400> SEQUENCE: 3129

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Phe Phe Val Asn Lys		1420
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